



XX WP1: 2001-343951/36.  
DR N-PSDB: AAS11602.  
XX  
XX Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,  
PT useful for preventing, diagnosing and treating e.g. eye disease,  
PT especially cataract formation -  
PS  
PS Chain 11; Fig 1; 16ppp; English.  
XX  
XX The invention relates to nucleic acids from human chromosome 2p21-16.3  
CC and the encoded peptide (and mouse and chicken orthologues) that  
CC comprises a PGECCPP group, an insulin-like growth factor binding protein  
CC (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group  
CC and a transmembrane domain. The protein, e.g. CRMI1, interacts with  
CC peptides of the transforming growth factor superfamily. A composition  
CC comprising an expression construct comprising the nucleic acids of the  
CC invention or a mimetic which antagonises or mimics an activity of the  
CC polypeptide may be used in a method for modulating the biological  
CC activity of a polypeptide of the bone morphogenic protein (BMP) family.  
CC In this way they may be used to prevent or treat an eye disease,  
CC especially cataract formation. They may also be used to treat  
CC neurodegenerative diseases, renal and kidney disease, bone and tooth  
CC abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in  
CC gene therapy by using antibodies directed against CRMI1 polypeptides.  
CC The present sequence represents mouse CRMI1 (AKA S52).  
XX  
XX Sequence 1037 AA:  
SQ  
Query Match 90.8%; Score 5402.5; DB 22; Length 1037;  
Best Local Similarity 88.5%; Pred. No. 6,7e+300;  
Matches 918; Conservative 51; Mismatches 67; Indels 1; Gaps 1;  
Dy 1 MYTVAGDRIAGAGCHLTVSLTLLTLLPSTGTRALVLPDDESKCEPFRNRPSSIVGYG 60  
Dy 1 MYTVAGGRIAGAGCHLTVSLTLLTLLPSTGTRALVLPDDESKCEPFRNRPSSIVGYG 60  
Qy 61 GCCTCAAGAGNCGSCGTFEGYXGQDGRGRCVYIRPLNGSDSTMYVAGVCEDEMTDQLL 120  
Db 61 GCCTCAAGAGNCGSCGATGAGCDGRGRCVYIRPLNGSDSTMYVAGVCEDEMTDQLL 120  
Qy 121 GPRPCNENIANGCNTINGKCECTCTCTCSNPFEPSPDMDLSTKRIEKPDCSKACE 180  
Db 121 GPRPCNENIANGCNTINGKCECTCTCTCSNPFEPSPDMDLSTKRIEKPDCSKACE 180  
Qy 181 YQSPSPCEPDSTVLEDTAPRGECCLPSPKVCINAGCLKAVCPQMLNIVSKSGPGE 240  
Db 181 YQSPSPCEPDSTVLEDTAPRGECCLPSPKVCINAGCLKAVCPQMLNIVSKSGPGE 240  
Qy 241 CCLLYACKRVGNQCNKRVYVQGTACAPPSVSEYQRLTADCCCTPFRDCISGICGF 300  
Db 241 CCLLYACKRVNPSDSTVEDCPVQVQANCLDSTEVRLTADCCCTPFRDCISGICGF 300  
Qy 301 PVECVGSTRVATSKSGDGTBKACDVFECYNDTKACVFNNAVETVGDGDFRNDNRFRCQ 360  
Db 301 PVECVGSTRVATSKSGDGTBKACDVFECYNDTKACVFNNAVETVGDGDFRNDNRFRCQ 360  
Qy 361 GGVALCFTAGCCEINCEKRYTPRGECPCVCEDDPYVFPNNPAGCTANGLLAHGRRKED 420  
Db 361 GGVALCFTAGCCEINCEKRYTPRGECPCVCEDDPYVFPNNPAGCTANGLLAHGRRKED 420  
Qy 421 CTFQCVCVNGERHCAVAVGQTCINPVKRVGECPCVCEPTLITVDPACGELSNCTLRK 480  
Db 421 CTFQCVCVNGERHCAVAVGQTCINPVKRVGECPCVCEPTLITVDPACGELSNCTLRK 480  
Qy 481 DCINGFRKDHNGCIRTCCINTDGLSKERRQGTINCFPGFLITDAQNCETICECRPKKCR 540  
Db 481 DCVYAGKRIKDHNGCIRTCCINTDGLSKERRQGTINCFPGFLITDAQNCETICECRPKKCR 540  
Qy 541 PTICDVFCEPLGLKLNKHCDDICRCKKCPRLSCIKICPLGFDQDSDHGLCLCRKSNASAG 600  
Db 541 PTICDVFCEPLGLKLNKHCDDICRCKKCPRLSCIKICPLGFDQDSDHGLCLCRKSNASAG 600